NUCLEIC ACID ANALYSIS TECHNIQUES

ABSTRACT OF THE DISCLOSURE

The present invention provides a simplified method for identifying differences in nucleic acid abundances (*e.g.*, expression levels) between two or more samples. The methods involve providing an array containing a large number (*e.g.* greater than 1,000) of arbitrarily selected different oligonucleotide probes where the sequence and location of each different probe is known. Nucleic acid samples (*e.g.* mRNA) from two or more samples are hybridized to the probe arrays and the pattern of hybridization is detected. Differences in the hybridization patterns between the samples indicates differences in expression of various genes between those samples. This invention also provides a method of end-labeling a nucleic acid. In one embodiment, the method involves providing a nucleic acid, providing a labeled oligonucleotide and then enzymatically ligating the oligonucleotide to the nucleic acid. Thus, for example, where the nucleic acid is an RNA, a labeled oligoribonucleotide can be ligated using an RNA ligase. In another embodiment, the end labeling can be accomplished by providing a nucleic acid, providing labeled nucleoside triphosphates, and attaching the nucleoside triphosphates to the nucleic acid using a terminal transferase.